## SEQUENCE LISTING

- 5 (i) APPLICANT: Ashkenazi, Avi J.

  Baker, Kevin
  Chuntharapai, Anan
  Gurney, Austin
  Kim, Kyung Jin
  Wood, William
  - (ii) TITLE OF INVENTION: Apo-2DcR
  - (iii) NUMBER OF SEQUENCES: 13

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- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genentech, Inc.
  - (B) STREET: 1 DNA Way
  - (C) CITY: South San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94080
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: WinPatin (Genentech)
- 30 (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 12-Jun-1998
  - (C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:

	(viii)	ATTORN	IEY/A	GENT	INE	ORMA	MOITA	J:						
5		(A) NA	ME:	Mars	char	ng, I	)iane	Ŀ L.						
		(B) RE	GIST	'RAT I	ON N	UMBE	ER: 3	5,60	0					
		(C) RE	FERE	NCE/	'DOCI	KET 1	IUMBE	ER: F	21110	)P1				
	(ix)	TELECO	NUMMC	IICAT	CION	INFO	RMAT	CION:						
10		(A) TE	ELEPH	ONE:	650	)/225	5-541	-6						
		(B) TE	ELEFA	X: 6	550/9	952-9	881							
	(2) IN	FORMATI	ON F	OR S	SEQ I	ID NO	):1:							
	(i)	SEQUEN	ICE C	CHAR <i>I</i>	ACTE	RISTI	CS:							
15		(A) LE	ENGTH	I: 25	59 ar	nino	acio	ds						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		(B) TY	PE:	Amir	no Ad	cid								
		(D) TC	POLC	GY:	Line	ear								
or the state of th														
	(xi)	SEQUEN	ICE I	DESC	RIPT	ION:	SEQ	ID I	10:1	:				
20	Mat A	la Arg	т] _	Dxo	Tara	Thr.	T 011	Tuc	Phe	U a l	U = I	Val	Tle	Val
	met A	ia Aig	116	5	пуъ	1111	пеа	шуз	10	val	vai	Vai	110	15
	_			J										
	Ala V	al Leu	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg
25				20					25					30
	Gln G	lu Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	
				35					40					45
30	His S	er Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser
			1	50			•		55	-				60
	Glu H	is Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Туз
				65					70					75
35														

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

	Thr	Asn	Ala	Ser	Asn 80	Asn	Glu	Pro	Ser	Cys 85	Phe	Pro	Cys	Thr	Val 90
5	Cys	Lys	Ser	Asp	Gln 95	Lys	His	Lys	Ser	Ser 100	Cys	Thr	Met	Thr	Arg 105
	Asp	Thr	Val	Cys	Gln 110	Cys	Lys	Glu	Gly	Thr 115	Phe	Arg	Asn	Glu	Asn 120
10	Ser	Pro	Glu	Met	Cys 125	Arg	Lys	Cys	Ser	Arg 130	Cys	Pro	Ser	Gly	Glu 135
15 🗇	Val	Gln	Val	Ser	Asn 140	Cys	Thr	Ser	Trp	Asp 145	Asp	Ile	Gln	Cys	Val 150
	Glu	Glu	Phe	Gly	Ala 155	Asn	Ala	Thr	Val	Glu 160	Thr	Pro	Ala	Ala	Glu 165
20	Glu	Thr	Met	Asn	Thr 170	Ser	Pro	Gly	Thr	Pro 175	Ala	Pro	Ala	Ala	Glu 180
20 mg ling to the line of the	Glu	Thr	Met	Asn	Thr 185	Ser	Pro	Gly	Thr	Pro 190	Ala	Pro	Ala	Ala	Glu 195
25	Glu	Thr	Met	Thr	Thr 200	Ser	Pro	Gly	Thr	Pro 205	Ala	Pro	Ala	Ala	Glu 210
2.0	Glu	Thr	Met	Thr	Thr 215	Ser	Pro	Gly	Thr	Pro 220	Ala	Pro	Ala	Ala	Glu 225
30	Glu	Thr	Met	Thr	Thr 230	Ser	Pro	Gly	Thr	Pro 235	Ala	Ser	Ser	His	Tyr 240
35	Leu	Ser	Cys	Thr	Ile 245	Val	Gly	Ile	Ile	Val 250	Leu	Ile	Val	Leu	Leu 255

	Ile	e Va	al :	Phe	Val	1
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5	(2)	IN	FOR	MATI	ION	
		(i)	SE	QUEI	1CE	,
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FOR SEQ ID NO:2:

- CHARACTERISTICS:
  - (A) LENGTH: 1180 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 <u> </u>	GCTGTGGGAA	CCTCTCCACG	CGCACGAACT	CAGCCAACGA	TTTCTGATAG	50
	ATTTTTGGGA	GTTTGACCAG	AGATGCAAGG	GGTGAAGGAG	CGCTTCCTAC	100
Total Live State	CGTTAGGGAA	CTCTGGGGAC	AGAGCGCCCC	GGCCGCCTGA	TGGCCGAGGC	150
20 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 =	AGGGTGCGAC	CCAGGACCCA	GGACGGCGTC	GGGAACCATA		5
21. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					Met 1	

GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Ile 5 10

GTC GCG GTC CTG CCA GTC CTA GCT TAC TCT GCC ACC 273 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr 25 15 20

ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala 30 35 40

-88-

	CCA	CAG	CAA	CAG	AGG	CAC	AGC	TTC	AAG	GGG	GAG	GAG	TGT	351
	Pro	Gln	Gln	Gln	Arg	His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	
					45					50				
5	CCA	GCA	GGA	TCT	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	390
	Pro	Ala	Gly	Ser	His	Arg	Ser	Glu	His	Thr	Gly	Ala	Cys	
		55					60					65		
	AAC	CCG	TGC	ACA	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	429
10	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	
				70					75					
	AAC	AAT	GAA	CCT	TCT	TGC	TTC	CCA	TGT	ACA	GTT	TGT	AAA	468
	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	
15	80					85					90			
	TCA	GAT	CAA	AAA	CAT	AAA	AGT	TCC	TGC	ACC	ATG	ACC	AGA	507
: M	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
			95					100					105	
1. man 1. man 1. man 1. man	GAC	ACA	GTG	TGT	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	546
5.63.1 10.11 10.11 10.11	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	
					110					115				
25	GAA	AAC	TCC	CCA	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	585
	Glu	Asn	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	
		120					125					130		
	CCT	AGT	GGG	GAA	GTC	CAA	GTC	AGT	TAA	TGT	ACG	TCC	TGG	624
30	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	
				135					140					
											GCC			663
	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	
35	145					150					155			

	ACT	GTG	GAA	ACC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	702
	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
			160					165					170	
5	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	741
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
					175					180				
	AAC	ACC	AGC	CCA	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	780
10	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		185					190					195		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	819
	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	
15 -				200			_		205					
100	GAA	GAG	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	858
	Glu	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	
	210					215					220			
20 <sup>1</sup>														
20	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	897
	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	
			225					230					235	
25	GCC	TCT	TCT	CAT	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	936
	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	
					240					245				
	ATA	GTT	CTA	ATT	GTG	CTT	CTG	ATT	GTG	TTT	GTT	Т 9	70	
30	Ile	Val	Leu	Ile	Val	Leu	Leu	Ile	Val	Phe	Val			
		250					255				259			
	GAA	AGAC'	TTC Z	ACTG'	TGGA.	AG A	AATT	CCTT	C CT	TACC'	TGAA	AGG	TTCA	GGT 1020
35	AGG	CGCT	GGC '	TGAG	GGCG	GG G	GGCG	CTGG	A CA	CTCT	CTGC	CCT	GCCT	CCC 1070

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TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAA 1120	
АДАДАДАДА ДАДАДАДАД АДАДАДАДА ДАДАДАДАД	
AAAAAAAAA 1180	
2) INFORMATION FOR SEQ ID NO:3:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 299 amino acids</li><li>(B) TYPE: Amino Acid</li><li>(D) TOPOLOGY: Linear</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly -40 -35 -30	
Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro	

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25 -15 -25 -20 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro 5 -5 1 -10 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro 20 15 10 Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Val Pro 35 25 30 30

Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
55 60 65

	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr 75	Thr	Asn	Ala	Ser	Asn 80
5	Asn	Glu	Pro	Ser	Cys 85	Phe	Pro	Cys	Thr	Val 90	Cys	Lys	Ser	Asp	Gln 95
	Lys	His	Lys	Ser	Ser 100	Cys	Thr	Met	Thr	Arg 105	Asp	Thr	Val	Cys	Gln 110
10	Cys	Lys	Glu	Gly	Thr 115	Phe	Arg	Asn	Glu	Asn 120	Ser	Pro	Glu	Met	Cys 125
1 <del>4</del>	Arg	Lys	Cys	Ser	Arg 130	Cys	Pro	Ser	Gly	Glu 135	Val	Gln	Val	Ser	Asn 140
	Cys	Thr	Ser	Trp	Asp 145	Asp	Ile	Gln	Cys	Val 150	Glu	Glu	Phe	Gly	Ala 155
20	Asn	Ala	Thr	Val	Glu 160	Thr	Pro	Ala	Ala	Glu 165	Glu	Thr	Met	Asn	Thr 170
	Ser	Pro	Gly	Thr	Pro 175	Ala	Pro	Ala	Ala	Glu 180	Glu	Thr	Met	Asn	Thr 185
25	Ser	Pro	Gly	Thr	Pro 190	Ala	Pro	Ala	Ala	Glu 195	Glu	Thr	Met	Thr	Thr 200
30	Ser	Pro	Gly	Thr	Pro 205	Ala	Pro	Ala	Ala	Glu 210	Glu	Thr	Met	Thr	Thr 215
30	Ser	Pro	Gly	Thr	Pro 220	Ala	Pro	Ala	Ala	Glu 225	Glu	Thr	Met	Thr	Thr 230
35	Ser	Pro	Gly	Thr	Pro 235	Ala	Ser	Ser	His	Tyr 240	Leu	Ser	Cys	Thr	Ile 245

	(2) I	NFOF	ITAMS	ON F	FOR S	SEQ I	D NC	):4:						
5	(i	( P	A) LE	ICE C	H: 11	.80 k	ase	pair	s					
			•	PE:										
				RANI				gle						
10		(1	); TC	POLC	)GY:	Line	ear							
	(xi	L) SE	EQUEN	ICE I	DESCF	RIPTI	ON:	SEQ	ID 1	10:4:	:			
15	GCTC	GTGG(	GAA (	CCTCI	rcca(	CG CC	GCACC	GAACI	CAC	GCCAA	ACGA	TTTO	CTGAT	AG 50
	חייים	rttga	GA (	ያ የተሞሞር	BACCA	AG AC	3	ATG	CAA	GGG	GTG	AAG	GAG	90
												Lys		
20								-40		-		_	-35	
and personal and an analysis of the second s	CGC	TTC	CTA	CCG	TTA	GGG	AAC	TCT	GGG	GAC	AGA	GCG	CCC	129
	Arg	Phe	Leu	Pro	Leu -30	Gly	Asn	Ser	Gly	Asp -25	Arg	Ala	Pro	
25	CGG	CCG	CCT	GAT	GGC	CGA	GGC	AGG	GTG	CGA	CCC	AGG	ACC	168
												Arg		
		-20		_			-15					-10		
	CAG	GAC	GGC	GTC	GGG	AAC	CAT	ACC	ATG	GCC	CGG	ATC	CCC	207
30	Gln	Asp	Gly	Val	Gly	Asn	His	Thr	Met	Ala	Arg	Ile	Pro	
				-5					1				5	
												GTC		246
	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val	Ala	Val	Leu	
35					10					15				

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val

250

255

	CTG	CCA	GTC	CTA	GCT	TAC	TCT	GCC	ACC	ACT	GCC	CGG	CAG	285
	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg	Gln	
		20					25					30		
5	GAG	GAA	GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	324
	Glu	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	
				35					40					
	AGG	CAC	AGC	TTC	AAG	GGG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	363
10	Arg	His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	
	45					50					55			
	CAT	AGA	TCA	GAA	CAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	402
	His	Arg	Ser	Glu	His	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	
15			60					65					70	
	GAG	GGT	GTG	GAT	TAC	ACC	AAC	GCT	TCC	AAC	AAT	GAA	CCT	441
	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	
					<b>7</b> 5					80				
20														
			TTC											480
	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp		Lys	
The state of the s		85					90					95		
														~ <b>.</b> .
25			AGT											519
	His	Lys	Ser		Cys	Thr	Met	Thr		Asp	Thr	vaı	Cys	
				100					105					
	CAG	TGT	AAA	GAA	GGC	ACC	TTC	CGG	AAT	GAA	AAC	TCC	CCA	558
30	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	
	110					115					120			
	GAG	ATG	TGC	CGG	AAG	TGT	AGC	AGG	TGC	CCT	AGT	GGG	GAA	597
	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	
35			125					130					135	

	GTC	CAA	GTC	AGT	AAT	TGT	ACG	TCC	TGG	GAT	GAT	ATC	CAG	636
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	
					140					145				
5	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	ACT	GTG	GAA	ACC	675
	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	
		150					155					160		
	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCG	GGG	ACT	714
10	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	
				165					170					
	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCA	753
	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	
15🗐	175					180					185			
	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	792
	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
			190					195					200	
ST. STATE	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	831
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
					205					210				
25	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	870
	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		215					220					225		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	TCT	TCT	CAT	909
30	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	
				230					235					
	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	ATA	GTT	CTA	ATT	948
	Tyr	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	
35	240					245					250			

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Ile Val Phe Val
255 259

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 43 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43
- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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## CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

	(2) INFORMATION FOR SEQ ID NO:7:													
5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 49 amino acids</li><li>(B) TYPE: Amino Acid</li><li>(D) TOPOLOGY: Linear</li></ul>													
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:													
	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His													
15	Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly 20 25 30													
20	Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys													
	Gly Cys Arg Lys 49													
25	(2) INFORMATION FOR SEQ ID NO:8:													
<i>23</i>	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 48 amino acids</li><li>(B) TYPE: Amino Acid</li><li>(D) TOPOLOGY: Linear</li></ul>													
30														
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:													
	Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn													

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln 20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
35 40 45

Cys Lys Glu

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- 10 (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 70 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1799 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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	CCCA	ACGCC	FTC (	JGCAT	('AAA')	.C Ac	CACC		۔ کی	AGAF	ICCC	CGCF	MICI	C1 30
	GCG(	CCCAC	CAA A	ATA	CACCO	SA CO	GATGO	CCCGA	A TCI	TACTI	TAA	GGGC	TGAA	AC 100
5	CCA	CGGG	CCT (	GAGAC	SACTA	AT A	AGAGO	CGTTC	C CCI	TACCO	FCC	ATG Met		145
												Δ.		
	CAA	CGG	GGA	CAG	AAC	GCC	CCG	GCC	GCT	TCG	GGG	GCC	CGG	184
10	Gln	Arg	Gly	Gin	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	
			5					10					15	
	AAA	ÄĠĠ	CAC	GGC	CCA	GGA	CCC	AGG	GAG	GCG	CGG	GGA	GCC	223
	Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	
15 <u> </u>					20					25				
Section 1	AGG	CCT	GGG	CTC	CGG	GTC	CCC	AAG	ACC	CTT	GTG	CTC	GTT	262
	Arg	Pro	Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	
15		30					35					40		
277 277 277	GTC	GCC	GCG	GTC	CTG	CTG	TTG	GTC	TCA	GCT	GAG	TCT	GCT	301
	Val	Ala	Ala	Val	Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	
				45					50					
25	CTG	ATC	ACC	CAA	CAA	GAC	CTA	GCT	CCC	CAG	CAG	AGA	GCG	340
	Leu	Ile	Thr	Gln	Gln	Asp	Leu	Ala	Pro	Gln	Gln	Arg	Ala	
	55					60					65			
	GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	GAG	GGA	TTG	379
30	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	Pro	Ser	Glu	Gly	Leu	
			70					75					80	
	TGT	CCA	CCT	GGA	CAC	CAT	ATC	TCA	GAA	GAC	GGT	AGA	GAT	418
	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	
35					85					90				

	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	457
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
		95					100					105		
<b>-</b> -	maa	יום אל ול	an a	CITIC!	C/mm	mm/d	TOC	ጥጥረ	ccc	ጥርር	እሮሮ	እርር	ጥርም	196
5												AGG		490
	Trp	Asn	Asp		ьeu	Pne	Cys	ьеи		Cys	TIIL	Arg	Cys	
				110					115					
	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
10	Asp	Ser	Gly	Glu	Vai	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
	120					125					130			
												TTC		574
	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe		
15			135					140					145	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2														
												CGC		613
	Glu	Glu	Asp	Ser		Glu	Met	Cys	Arg		Cys	Arg	Thr	
					150					155				
							~~~		ama	aam	C T C	mam	2 (2)	<b>CE</b> 2
1001 1001 1001 1001 1001 1001 1001 100												TGT		652
10 m	GLy		Pro	Arg	GLY	Met		Lys	vaı	GTA	Asp	Cys	THE	
<u> </u>		160					165					170		
25	ccc	TCC	አርጥ	CAC	እጥሮ	C N N	ጥርረጥ	ርጥር	$C\Delta C$	<b>2</b>	GAA	TCA	GGC	691
25												Ser		-
	110	115	001	175	110	Ora	Cyb	val	180	210			1	
				1,5										
	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
30	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
	185					190					195			
	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
35			200					205					210	

	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
					215					220				
5	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
		225					230					235		
1	GGG	GCT	GAG	GAC	TAA	GTC	CTC	TAA	GAG	ATC	GTG	AGT	ATC	886
LO	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240					245					
													GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
15	250					255					260			
													TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu		
			265					270					275	
20												~	~ ~ ~	
														1003
### ### ####	Pro	Gly	Glu	Ser		His	Leu	Leu	Glu		Ala	Glu	Ala	
int.					280					285				
	~	* ~ ~		G3.G	3.00	3.00	3.00	ama	ama	CITIES .		CCA	יח א א	1042
25														1042
	GIu	_	Ser	GIn	Arg	Arg		ьeu	ьeu	vai	Pro	Ala	ASII	
		290					295					300		
	(1 N N	aam	C174 (T1)	aaa	<b>7</b> . CT	CAC	አ ረጥ	CTC	አ ር አ	CAC	ሞርር	ጥጥር	CAT	1081
2.0														1001
30	Glu	GIY	Asp		TIII	GIU	1111	пеп	310	GIII	Cys	Phe	Asp	
				305					310					
	GAC	արդու	CCA	GAC	ጥጥር፤	СТС	רככ	փփփ	GAC	ጥሮሮ	ፐርር	GAG	CCG	1120
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35	315	THE	ALG	7100	Leu	320	110			~~1	325		- 2 0	
J J	シェン													

CTC	ATG	AGG	AAG	TTG	GGC	CTC	ATG	GAC	TAA	GAG	ATA	AAG	1159	9
Leu	Met	Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys		
		330					335					340		
GTG	GCT	AAA	GCT	GAG	GCA	GCG	GGC	CAC	AGG	GAC	ACC	TTG	119	8
Val	Ala	Lys	Ala	Glu	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu		
				345					350					
														_
													123	7
Tyr	Thr	Met	Leu	Ile	Lys	Trp	Val	Asn	Lys	Thr		Arg		
	355					360					365			
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													127	O
Asp	Ala	Ser		HIS	Thr	ьeu	Leu		Ala	ьеи	Giu	1111		
			370					375						
OTT-C	CCA	CAC	אכא	CTT	CCC	λλC	CAG	ΔΔG	ידידע	GAG	GAC	CAC	131	5
														_
	GIY	Giu	Arg	Беа		цур	0111	цур	110		1101			
300					303									
TTG	TTG	AGC	TCT	GGA	AAG	TTC	ATG	TAT	CTA	GAA	GGT	AAT	135	4
		395		_	_		400					405		
GCA	GAC	TCT	GCC	WTG	TCC	TAA	GTGT	G AT	TCTC	TTCA	GGA	AGTG.	AGA	1400
Ala	Asp	Ser	Ala	Xaa	Ser									
				410	411									
CCT	TCCC	TGG	TTTA	CCTT	TT T	TCTG	GAAA	A AG	CCCA	ACTG	GAC	TCCA	GTC	1450
AGT	AGGA	AAG	TGCC	ACAA	TT G	TCAC	ATGA	.C CG	GTAC	TGGA	AGA	AACT	CTC	1500
							~-	m aa		3 CO	mmo	13 CMC	C2 C	1550
CCA	TCCA	ACA	TCAC	CCAG	TG G	ATGG	AACA	T CC	TGTA	AC'1"I	Turc	ACTG	CAC	1220
~	~~~ <del>_</del>	m 3 m	നന്ദ്രനസ	י <b>דרוו</b> דו	aa m	רות א מות	CTTC N	ת תייחי	ጥ አ አ ጥ	ייי א רייא	ርጥ እ	ጥርረን	ጉልጥ	1600
TTG	GCA'I'	TAT	T.I.I.I.	ATAA	GC T	GAAT	GIGA	.ı AA	LAAU	CACA	. CIA	LIGGA	LT.T.	1000
	GTG Val  TAC Tyr  GAT Asp  CTG Leu 380  TTG Leu GCA Ala  CCT AGT	Heu Met  GTG GCT Val Ala  TAC ACG Tyr Thr 355  GAT GCC Asp Ala  CTG GGA Leu Gly 380  TTG TTG Leu Leu  GCA GAC Ala Asp  CCTTCCC  AGTAGGA  CCATCCA	Leu Met Arg 330  GTG GCT AAA Val Ala Lys  TAC ACG ATG Tyr Thr Met 355  GAT GCC TCT Asp Ala Ser  CTG GGA GAG Leu Gly Glu 380  TTG TTG AGC Leu Leu Ser 395  GCA GAC TCT Ala Asp Ser  CCTTCCCTGG  AGTAGGAAAG	Leu Met Arg Lys   330 Ser AAA GCT   Val Ala Lys Ala   TAC ACG ATG CTG   Tyr Thr Met Leu   355 Ser Val   CTG GGA TCT GTC   Asp Ala Ser Val   370 AGA AGA AGA   Leu Gly Glu Arg   380 TCT AGC TCT   Leu Leu Ser Ser   395 Ser Ala   CCTTCCCTGG TTTA   AGTAGGAAAG TGCC   CCATCCAACA TCAC	Leu Met Arg Lys Leu   330 GTG GAG   Wal Ala Lys Ala Glu   Val Ala Lys Ala Glu   345   TAC ACG ATG CTG ATA   Tyr Thr Met Leu Ile   355 Leu GTC CAC   Asp Ala Ser Val His   370 His 370 CTT   CTG GGA GAG AGA CTT   Leu Gly Glu Arg Leu   380 TCT GGA   Leu Leu Ser Ser Gly   395 GCA GCC WTG   Ala Asp Ser Ala Xaa   410   CCTTCCCTGG TTTACCTA   AGTAGGAAAG TGCCCACAA   CCATCCAACA TCACCCAG	Leu Met Arg Lys Leu Gly   GTG GCT AAA GCT GAG GCA   Val Ala Lys Ala Glu Ala   TAC ACG ATG CTG ATA AAG   Tyr Thr Met Leu Ile Lys   355 GAT CAC ACC   Asp Ala Ser Val His Thr   370 TTG GCA ACC ACC   Leu Gly Glu Arg Leu Ala   380 TCT GGA AAG AAG   Leu Leu Ser Ser Gly Lys   395 GCA GAC TCT GCC WTG TCC   Ala Asp Ser Ala Xaa Ser   410 411 AGTAGGAAAG TGCCACAAATT GCCACCACAATT GCCATCCAACA TCACCCAGTG GCCATCCAACA TCACCCAGTG GCCATCCAACA TCACCCCAGTG GCCACCACACT	Leu Met Arg Lys Leu Gly Leu 330    GTG GCT AAA GCT GAG GCA GCG Val Ala Lys Ala Glu Ala Ala Ala 345    TAC ACG ATG CTG ATA AAG TGG Tyr Thr Met Leu Ile Lys Trp 355    GAT GCC TCT GTC CAC ACC CTG Asp Ala Ser Val His Thr Leu 370    CTG GGA GAG AGG CTT GCC AAG Leu Gly Glu Arg Leu Ala Lys 380    TTG TTG AGC TCT GGA AAG TTC Leu Leu Ser Ser Gly Lys Phe 395    GCA GAC TCT GCC WTG TCC TAA Ala Asp Ser Ala Xaa Ser 410 411    CCTTCCCTGG TTTACCTTTT TTCTG AGTAGAACA TGCCATCCAACA TCACCCAGTG GATGG	Leu         Met         Arg         Lys         Leu         Gly         Leu         Met           330         GCT         GAG         GCA         GCG         GGC           Val         Ala         Lys         Ala         Glu         Ala         Ala         Gly           TAC         ACG         ATG         CTG         ATA         AAG         TGG         GTC           TYr         Thr         Met         Leu         Ile         Lys         Trp         Val           355         TCT         GTC         CAC         ACC         CTG         CTG           GAT         GCC         TCT         GTC         CAC         ACC         CTG         CTG           Asp         Ala         Ser         Val         His         Thr         Leu         Leu         Leu         Leu         Leu         Ala         Lys         Gln         Ala         Lys         Gln         Ala         Ala	Leu Met Arg Lys Leu Gly Leu Met Asp 330 Asp 335   GTG GCT AAA GCT GAG GCA GCG GGC CAC Val Ala Lys Ala Glu Ala Ala Gly His 345 Ala Glu Ala Ala Gly Ala Gly His 345   TAC ACG ATG CTG ATA AAG TGG GTC AAC Tyr Phr Met Leu Ile Lys Trp Val Asn 360 Asn 360   GAT GCC TCT GTC CAC ACC CTG CTG GAT Asp Ala Ser Val His Thr Leu Leu Asp 370 AGT GCA GAG AGA CTT GCC AAG CAG AAG Leu Gly Glu Arg Leu Ala Lys Gln Lys 380   TTG TTG AGC TCT GGA AAG TTC ATG TAT Leu Leu Ser Ser Gly Lys A95 AGT AGA TCT GCC WTG TCC TAAGTGTG ATA A1a Asp Ser Ala Xaa Ser 410 411   GCA GAC TCT GCC WTG TCC TAAGTGTG ATA AGTAGAAAAA AGGAGTAGGAAAAA TCACCCACTT GATGAACAT CCCTTCCAACA TCACCCAGTG GATGAACAT CCCATCCAACA TCACCCAGTG GATGAACAT CCCATCCAACA TCACCCAGTG GATGAACAT CCCATCAACA TCACCCAGTG GATGAACAT CCCATCAACA TCACCCAGTG GATGAACAT CCCATCACA TCACCCAGTG GATGAACAT CCCATCAACA TCACCCAGTG GATGAACAT CCCATCACA TCACCCAGTG GATGAACAT CCCATCACATCA	Heu Met Arg Lys Leu Gly Leu Met Asp Asn 330	Heu Met Arg Lys Leu Gly Leu Met Asp Asn Glu 330	Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile 330	Leu   Met   Arg   Lys   Leu   Gly   Leu   Met   Asp   Asn   Glu   Ile   Lys   340	330

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650 TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAA AAAAAAAAA 1750 5 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799 (2) INFORMATION FOR SEQ ID NO:11: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg 15 10 5 1 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro 25 30 20 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val 45 40 35 25 Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp 55 60 50

35

30

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp

65

80

70

85

75

	Gly Ar	g Asp	Cys	Ile 95	Ser	Cys	Lys	Tyr	Gly 100	Gln	Asp	Tyr	Ser	Thr 105
5	His Tr	p Asn	Asp	Leu 110	Leu	Phe	Cys	Leu	Arg 115	Cys	Thr	Arg	Cys	Asp 120
	Ser Gl	y Glu	Val	Glu 125	Leu	Ser	Pro	Cys	Thr 130	Thr	Thr	Arg	Asn	Thr 135
10	Val Cy	s Gln	Cys	Glu 140	Glu	Gly	Thr	Phe	Arg 145	Glu	Glu	Asp	Ser	Pro 150
ž==t	Glu Me	t Cys	Arg	Lys 155	Cys	Arg	Thr	Gly	Cys 160	Pro	Arg	Gly	Met	Val 165
	Lys Va	l Gly	Asp	Cys 170	Thr	Pro	Trp	Ser	Asp 175	Ile	Glu	Cys	Val	His 180
20	Lys Gl	u Ser	Gly	Ile 185	Ile	Ile	Gly	Val	Thr 190	Val	Ala	Ala	Val	Val 195
	Leu Il	e Val	Ala	Val 200	Phe	Val	Cys	Lys	Ser 205	Leu	Leu	Trp	Lys	Lys 210
25	Val Le	eu Pro	Tyr	Leu 215	Lys	Gly	Ile	Cys	Ser 220	Gly	Gly	Gly	Gly	Asp 225
20	Pro Gl	u Arg	Val	Asp 230	Arg	Ser	Ser	Gln	Arg 235	Pro	Gly	Ala	Glu	Asp 240
30	Asn Va	al Leu	. Asn	Glu 245	Ile	Val	Ser	Ile	Leu 250	Gln	Pro	Thr	Gln	Val 255
35	Pro G	lu Gln	Glu	Met 260		Val	Gln	Glu	Pro 265		Glu	Pro	Thr	Gly 270

	Val	Asn	Met	Leu	Ser 275	Pro	Gly	Glu	Ser	Glu 280	His	Leu	Leu	Glu	Pro 285
5	Ala	Glu	Ala	Glu	Arg 290	Ser	Gln	Arg	Arg	Arg 295	Leu	Leu	Val	Pro	Ala 300
	Asn	Glu	Gly	Asp	Pro 305	Thr	Glu	Thr	Leu	Arg 310	Gln	Cys	Phe	Asp	Asp 315
10	Phe	Ala	Asp	Leu	Val 320	Pro	Phe	Asp	Ser	Trp 325	Glu	Pro	Leu	Met	Arg 330
15 🚡	Lys	Leu	Gly	Leu	Met 335	Asp	Asn	Glu	Ile	Lys 340	Val	Ala	Lys	Ala	Glu 345
	Ala	Ala	Gly	His	Arg 350	Asp	Thr	Leu	Tyr	Thr 355	Met	Leu	Ile	Lys	Trp 360
20	Val	Asn	Lys	Thr	Gly 365	Arg	Asp	Ala	Ser	Val 370	His	Thr	Leu	Leu	Asp 375
And the there will be the tenth	Ala	Leu	Glu	Thr	Leu 380	Gly	Glu	Arg	Leu	Ala 385	Lys	Gln	Lys	Ile	Glu 390
25	Asp	His	Leu	Leu	Ser 395	Ser	Gly	Lys	Phe	Met 400	Tyr	Leu	Glu	Gly	Asn 405
30	Ala	Asp	Ser	Ala		Ser 411									
	(2)	INFO	RMAT	ION :	FOR :	SEQ	ID N	0:12	:						
	(		EQUE A) L												

(B) TYPE: Nucleic Acid

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

(C) STRANDEDNESS: Single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

(D) TOPOLOGY: Linear